



PCT

RAW SEQUENCE LISTING

DATE: 02/11/2003

PATENT APPLICATION: US/10/018,248A

TIME: 14:35:12

Input Set : A:\10018248a.raw.txt

Output Set: N:\CRF4\02112003\J018248A.raw

3 <110> APPLICANT: EXELIXIS, INC.
5 <120> TITLE OF INVENTION: ANIMAL MODELS AND METHODS FOR ANALYSIS OF LIPID METABOLISM
AND SCREENING

6 OF PHARMACEUTICAL AND PESTICIDAL AGENTS THAT MODULATE LIPID METABOLISM
8 <130> FILE REFERENCE: EX99-004C-US
10 <140> CURRENT APPLICATION NUMBER: 10/018,248A
C--> 11 <141> CURRENT FILING DATE: 2002-07-30
13 <150> PRIOR APPLICATION NUMBER: US 60/189,700
14 <151> PRIOR FILING DATE: 2000-03-15
16 <150> PRIOR APPLICATION NUMBER: US 09/332,522
17 <151> PRIOR FILING DATE: 1999-06-14
19 <160> NUMBER OF SEQ ID NOS: 8
21 <170> SOFTWARE: PatentIn version 3.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 3419
25 <212> TYPE: DNA
26 <213> ORGANISM: Caenorhabditis elegans
28 <400> SEQUENCE: 1

p.6

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73	caattcaata	cactgaatac	tctgcccgat	caccgctcga	atcatctcct	tctccacct	1380
75	gaaatgagag	aaaacgatca	cgaatgagca	caacgactcc	tatgaagaat	ggaactagag	1440
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85 tatatgtggt tgtcaaaactg ctgatccatg gtgaccctgt tcaagacttc atgtccgctt 1740
87 catggcagac ttttgtgacg actcgagaga aggcgagagc cgagttgaac tctggaaatt 1800
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135 tctacgagct cacgtgccga atgctcaacg gagccaaccc acaagccacg tggtcaggcg 3240
137 yccgacgcgt tcgatctaca aaaatggacg cggctccagg aagagtgcgc atgcgacgct 3300
139 cggctcaacc ggacgcattt catcttcata cactggttaa actacatact tctatggatc 3360
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144 <210> SEQ ID NO: 2

145 <211> LENGTH: 1113

146 <212> TYPE: PRT

147 <213> ORGANISM: Caenorhabditis elegans

149 <220> FEATURE:

150 <221> NAME/KEY: misc_feature

151 <222> LOCATION: (1073)..(1073)

152 <223> OTHER INFORMATION: "X" is any amino acid

155 <400> SEQUENCE: 2

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162 20 25 30
165 Pro Leu Asp Phe Asp Met Glu His Asn Trp Gln Glu Pro Gly Pro Ser
166 35 40 45
169 Gln Gln Pro Asp Pro Ser Ile Pro Gly Asn Gln His Ser Pro Pro Gln
170 50 55 60
173 Glu Tyr Tyr Asp Ile Asp Gly Gln Arg Asp Val Ser Thr Leu His Ser
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178					85					90					95	
181	Pro	Asn	Phe	Asp	Leu	Gly	Gly	Gly	Arg	Gly	Pro	Ser	Leu	Ala	Ala	Thr
182				100					105					110		
185	Gln	Gln	Leu	Ser	Gly	Glu	Gly	Pro	Ala	Ser	Met	Leu	Asn	Pro	Leu	Gln
186			115					120					125			
189	Thr	Ser	Pro	Pro	Ser	Gly	Gly	Tyr	Pro	Pro	Ala	Asp	Ala	Tyr	Arg	Pro
190		130					135					140				
193	Leu	Ser	Leu	Ala	Gln	Gln	Leu	Ala	Ala	Pro	Ala	Met	Thr	Pro	His	Gln
194	145					150					155					160
197	Ala	Ala	Ser	Leu	Phe	Val	Asn	Thr	Asn	Gly	Ile	Asp	Gln	Lys	Asn	Phe
198					165					170					175	
201	Thr	His	Ala	Met	Leu	Ser	Ser	Pro	His	His	Thr	Ser	Met	Thr	Ser	Gln
202				180						185				190		
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206			195					200					205			
209	Asp	Gln	Ala	Gln	Gly	Pro	Ser	Gly	Pro	Ser	Tyr	Tyr	Ser	Gln	His	His
210		210					215					220				
213	Gln	Ser	Pro	Pro	Pro	His	His	His	His	His	His	Pro	Met	Pro	Lys	Ile
214	225					230					235					240
217	His	Glu	Asn	Pro	Glu	Gln	Val	Ala	Ser	Pro	Ser	Ile	Glu	Asp	Ala	Pro
218					245					250				255		
221	Glu	Thr	Lys	Pro	Thr	His	Leu	Val	Glu	Pro	Gln	Ser	Pro	Lys	Ser	Pro
222				260					265					270		
225	Gln	Asn	Met	Lys	Glu	Glu	Leu	Leu	Arg	Leu	Leu	Val	Asn	Met	Ser	Pro
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233	Thr	Asn	Gly	Pro	Ser	Arg	Ser	Lys	Glu	Lys	Ala	Ala	Lys	Ile	Val	Ile
234	305					310					315					320
237	Gln	Glu	Thr	Ala	Glu	Gly	Asp	Glu	Asp	Glu	Asp	Asp	Glu	Asp	Ser	Asp
238				325					330						335	
241	Ser	Gly	Glu	Thr	Met	Ser	Gln	Gly	Thr	Thr	Ile	Ile	Val	Arg	Arg	Pro
242				340					345					350		
245	Lys	Thr	Glu	Arg	Arg	Thr	Ala	His	Asn	Leu	Ile	Glu	Lys	Lys	Tyr	Arg
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249	Cys	Ser	Ile	Asn	Asp	Arg	Ile	Gln	Gln	Leu	Lys	Val	Leu	Leu	Cys	Gly
250		370				375						380				
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254	385					390					395					400
257	His	Ile	Glu	Glu	Val	Glu	His	Glu	Asn	Gln	Val	Leu	Lys	His	His	Val
258				405						410					415	
261	Glu	Gln	Met	Arg	Lys	Thr	Leu	Gln	Asn	Asn	Arg	Leu	Pro	Tyr	Pro	Glu
262				420					425					430		
265	Pro	Ile	Gln	Tyr	Thr	Glu	Tyr	Ser	Ala	Arg	Ser	Pro	Val	Glu	Ser	Ser
266			435					440					445			
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278				485						490					495	
281	Ala	Gly	Ser	Ala	Ile	Phe	Ser	Lys	Ala	Ala	Ala	Glu	Ala	Pro	Ile	Ala
282				500					505					510		
285	Ser	Pro	Phe	Glu	His	Gly	Arg	Val	Ile	Asp	Asp	Pro	Asp	Gly	Thr	Ser
286			515					520					525			
289	Thr	Arg	Thr	Leu	Phe	Trp	Glu	Gly	Ser	Ile	Ile	Asn	Met	Ser	Tyr	Val
290		530					535					540				
293	Trp	Val	Phe	Asn	Ile	Leu	Met	Ile	Ile	Tyr	Val	Val	Val	Lys	Leu	Leu
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297	Ile	His	Gly	Asp	Pro	Val	Gln	Asp	Phe	Met	Ser	Val	Ser	Trp	Gln	Thr
298				565						570					575	
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306			595					600					605			
309	Arg	Ser	Leu	Pro	Ser	Pro	Gly	Val	Asp	Ser	Val	Phe	Ser	Val	Gly	Trp
310		610					615					620				
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314	625					630					635					640
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322				660					665					670		
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334	705					710					715					720
337	Tyr	Ile	Ser	Ala	Ser	Ile	Gln	Cys	Arg	Leu	Ala	Leu	Pro	Asn	Leu	Leu
338				725						730					735	
341	Ala	Pro	Phe	Phe	Ser	Gly	Tyr	Phe	Leu	Arg	Arg	Ala	Arg	Arg	His	Val
342				740					745					750		
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346			755					760					765			
349	Pro	Ala	Thr	Arg	Lys	Phe	Met	Ser	Asp	Ala	Lys	Arg	Leu	Glu	His	Val
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358				805						810					815	
361	Leu	Leu	Ser	Lys	Leu	Val	Gln	Glu	Leu	Val	Gly	Gly	Asp	Glu	Ile	Phe
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366			835					840					845			
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378      885      890      895
381 His Val Leu Thr Cys Gly Ile Tyr Trp Arg Ser Asn Lys Asn Glu Leu
382      900      905      910
385 Ala Arg Gln His Tyr Ser Leu Ile Arg Asn Cys Pro Pro Lys Ile Leu
386      915      920      925
389 Thr Asp Asn Leu Gly Leu Ala Val Gly His Ala Leu Cys Ala Arg Lys
390      930      935      940
393 Ile Cys Ile Asp Asp Arg Asp Ser Pro Lys Val Ser Gln Tyr Val Cys
394 945      950      955      960
397 Ile His Thr Lys Lys Ser Leu Glu Ser Leu Arg Leu Phe Ser Thr Ser
398      965      970      975
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402      980      985      990
405 Met Ala Tyr Glu Trp Ile Met Asn Ser Leu Leu Asp Ala Trp Arg Ser
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409 Asn Leu Phe Ala Ser Lys Pro Tyr Trp Thr Gln Ser Phe Lys Gly
410      1010      1015      1020
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418      1040      1045      1050
421 Tyr Glu Leu Thr Cys Arg Met Leu Asn Gly Ala Asn Pro Gln Ala
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429 Val Arg Gly Arg Val Ser Met Arg Arg Ser Ala Gln Pro Asp Ala
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:7; N Pos. 3038,3049
Seq#:8; Xaa Pos. 993

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